

TITLE: MOSAIC INFECTIOUS BURSAL  
DISEASE VIRUS VACCINES  
Inventor: Boot et al.  
Serial No.: 10/046,671  
Docket No.: 2183-5238US

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**Fig.2a Alignment of IBDV A-segment cDNA sequences**

Consensus	GGATAGATC GGTCTGACC	CGGGGAGTC ACCGGGGAC	AGGCTGACAA GGTCTGTTC	CAGATGAAA CTCT	75
CEP94-A	.....	.....	...G.T... ..T.....	.....	75
D6948-A	.....	.....	...T.A... ..C.....	.....	75
TY89-A	.....	.....	.....	.....	75
Consensus	CCTTCTACAA TGTATCTTT	GATGTTTAT AGAGATCAGA	CNAAGATCG CAGGCTGAC	TAAGCTGCAA GATCA	150
CEP94-A	..... C.....	.....C.....	.....	..... A.....	150
D6948-A	..... T.....	.....F.....	.....	..... G.....	150
TY89-A	.....	.....	.....	.....	150
Consensus	AACCCACAG ATTGTTCCCT	TCATAGGAG CCTTCTGATG	CCAACACCG GACCGGGTC	CATTCCGAC GACAC	225
CEP94-A	.....	.....	.....	.....	225
D6948-A	.....	.....	.....	.....	225
TY89-A	.....	.....	.....	.....	225
Consensus	CCTGAGGAG CACACTCTCA	GTTCAGGAC CTCAGCTAC	AATTGACTG TGGGGGAC	AGGCTGAGG CTAT	300
CEP94-A	...G.....	.....	.....	.....	300
D6948-A	...A.....	.....	.....	.....	300
TY89-A	.....	.....	.....	.....	300
Consensus	TGTCTTTTC CCTGGTTCC	CTGCTCAAT TGTGGTGCT	CATTCACAC TCCAGGCAA	TGGAACTAC AGTT	375
CEP94-A	..... .A.....	.....	.....	.....	375
D6948-A	..... .T.....	.....	.....	.....	375
TY89-A	.....	.....	.....	.....	375
Consensus	CGATCAGAT CTCTGACTG	CCGAACTT ACCGGCCAG	TACACTACT GCAGCTTAT	GATCGAGT CTCAC	450
CEP94-A	.....	.....T.....	.....	.....	450
D6948-A	.....	.....C.....	.....	.....	450
TY89-A	.....	.....	.....	.....	450
Consensus	AGTGGGTCA AGCACTTC	CTGGTGGCT TTATGCACTA	AATGGACCA TAAAGCCCT	GACCTTCAA GGAG	525
CEP94-A	..... .T.....	.....	...C.....	.....	525
D6948-A	..... .C.....	.....	...T.....	.....	525
TY89-A	.....	.....	.....	.....	525
Consensus	CCTGAGTGA CTGACGATG	TTCCTACAA TGGGTGATG	TCTGCACAG CCAACATCA	GACAAATY GGGAA	600
CEP94-A	.....	.....	.....	.....T.....	600
D6948-A	.....	.....	.....	.....	600
TY89-A	.....	.....	.....	.....	600
Consensus	GCTCCATGA GGGGAGGGG	TACCTCTCT CAGCTTACC	ACATCATAT ATCTGGGTA	TGTAGACTY GGTGA	675
CEP94-A	.....	...C.....	.....	.....G..T.....	675
D6948-A	.....	...A.....	.....	.....A..C.....	675
TY89-A	.....	.....	.....	.....	675
Consensus	CCCATTCCT GCGATAGGC	TTCAGCCAA AATGTTAGC	ACATGTGCA GCAGTGACG	GCCAGAGTC TACAC	750
CEP94-A	..... .A.....	.....T.....	.....C.....	.....	750
D6948-A	..... .T.....	.....C.....	.....A.....	.....	750
TY89-A	.....	.....	.....	.....	750
Consensus	CATACTOCA GCGATGATT	ACCAATCTC ATCAGCTAC	CAACGAGTG GGTATACAT	CACACTGTC TCAGC	825
CEP94-A	.....	.....	...C.....	.....	825
D6948-A	.....	.....	...G.....	.....	825
TY89-A	.....	.....	.....	.....	825
Consensus	YAAATATGAT GCGATCACA	GCCTCAGCT TGGGGAGAR	CTGTTGTTT AAACAAGCT	CCAGGCTT RTACT	900
CEP94-A	C..C..T...	.....G..T.....	.....G.....	.....C.....G.....	900
D6948-A	T..T..C...	.....A..C.....	.....A.....	.....A.....A.....	900
TY89-A	.....	.....	.....	.....	900
Consensus	GGTGTCTACC ATCTACTTA	TAGCTTTGA TGGGACGCG	GTAATCACA GAGCTGTGC	GCGACACT GGGCT	975
CEP94-A	...C..C...	.....C.....	...A.....	...G.....A.....	975
D6948-A	...T..T...	.....T.....	...T.....	...A.....G.....	975
TY89-A	.....	.....	.....	.....	975

[illegible]

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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Fig. 2a Contd. Alignment of 180V A-B segment with B. subtilis										1050
Consensus	RACGRCGCG	ACTGACAACC	TTWTCGATT	CAATTTTGTG	ATTCCACGGA	RCGAGATTAAC	CCAGCCCAATC	ACATC		
CEP94-A	G...A...	..C.....	..T.....	...C.....	.....A.	A.....	.....	.....		1050
D6948-A	A...G....	..T.....	..A.....	...A.....	.....C.	G.....	.....	.....		1050
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CATCAAACTG	GAGATAGTGA	CCTCCAAAAG	TGGTGTTCAG	GCGGGGATC	AGATGTCTGT	GTCTGCCAGG	GCGAG		1125
CEP94-A	.....	.....	.....	.....	..A.....	.....G..	..G....A	.....		1125
D6948-A	.....	.....	.....	.....	..G.....	.....A..	..A....T	.....		1125
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CCTGACGATG	ACGATCCATG	GTGCAACTA	TCCAGGGGCC	CTCGGTCCGG	TCACCTTAGT	BGCTACGAA	AGAGT		1200
CEP94-A	.....	.....T.	.....	.....	.....	.....G..	G.....	.....		1200
D6948-A	.....	.....C.	.....	.....	.....	...A...	A.....	.....		1200
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GCGACACAGA	TCGTGTGTTA	CGGTGCGT	GGTGACAC	TTGAGCTGA	TCCCAATCC	TGACTAGCA	AGAA		1275
CEP94-A	.....	..C.....	.....T.	.....	.....	.....	.....	.....		1275
D6948-A	.....	..T.....	.....C.	.....	.....	.....	.....	.....		1275
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CCTGCTTACA	GAATACGGCC	GATTTCGCC	AGAGCCCATG	AACTACACAA	AATTGATCT	GATGTAGAGG	GACCG		1350
CEP94-A	.....T..	.....	.....	.....	.....	.....	.....	.....		1350
D6948-A	.....C..	.....	.....	.....	.....	.....	.....	.....		1350
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	TCCTGGCATC	AGAGCGGTTT	GGCCACACAG	GGGTACACT	GACTTTGCTG	AACTACTCAT	GGGGTGCC	GGCT		1425
CEP94-A	.....	.....C.	.....	.....	.....T.	..A.....	.....	.....		1425
D6948-A	.....	.....A.	.....	.....	.....C.	..G.....	.....	.....		1425
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CAACTCTGCC	CTGAGATG	CAGGCGATT	TGGCTTCAA	GACATATCC	GGCGCTTAG	GAGATAGCT	GTGCC		1500
CEP94-A	.....	.....	.....	.....T.	.....	.....A..	.....	.....		1500
D6948-A	.....	.....	.....	.....C.	.....	.....C..	.....	.....		1500
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GTTGTCTCT	ACATTGTTCC	CACCTGCGC	TCCCTAGCC	CATGCATG	GGGAGGTGT	AGACTACCTG	CTGGG		1575
CEP94-A	.....C..	..T.....	..T.....	.....	.....	.....	.....	.....		1575
D6948-A	.....T..	..C.....	..C.....	.....	.....	.....	.....	.....		1575
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CGATGAGGCA	CAGGCTCTT	CAGGAATGC	TGAGCGCGG	TCAGGAAAG	CAAGAGCTC	CTCAGCGGCC	ATAG		1650
CEP94-A	.....	.....	.....	.....	.....	.....	.....	.....		1650
D6948-A	.....	.....	.....	.....	.....	.....	.....	.....		1650
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GCGCTACT	CTGCGCGCG	ACAGGGTA	CGAGGTAGTC	GGAATCTTT	TTGAGGTCC	CCGAACTCT	GTAGT		1725
CEP94-A	.....G..	.....	.....	.....	.....A.	..C.....	.....C..	.....		1725
D6948-A	.....A..	.....	.....	.....	.....G.	..T.....	.....T..	.....		1725
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CGACGGAT	CTGCTTCAC	CTGGGTACT	CCGGGTGCA	CACAACTCG	ACTCGGTGT	BAGAGGGGT	GCCAC		1800
CEP94-A	.....	..T.....	.....G..	.....T..	.....	.....	A.....	.....		1800
D6948-A	.....	..C.....	.....A..	.....C..	.....	.....	G.....	.....		1800
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GCTATTCCCT	GTGTATATTA	CGACAGTGA	AGATGCCATG	ACNCCCAAG	CATGAAACAG	CAAAATGTTT	GCTGT		1875
CEP94-A	.....	.....T..T.	.....	..C.....	.....	..T.....	.....	.....		1875
D6948-A	.....	.....C..C.	.....	..T.....	.....	..C.....	.....	.....		1875
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CATTGAGGC	GTGCGAGAG	ATCTCCAAAC	TCCATCTCAA	AGAGGATCT	TCAACAGAC	TCTCTCTGGA	CATAG		1950
CEP94-A	.....	.....	..C.....	..T.....	.....	.....	.....T..	..C.....		1950
D6948-A	.....	.....	..T.....	..A.....	.....	.....	.....C..	..T.....		1950
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		

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Fig.2a Contd. Alignment of IBV A-segment cDNA sequences

Consensus	AGTCATGGA TATGCTCCAG ATGGGTTACT TCCACTGGAG ACTGGGAGAG ATTACACCGT KOTCCCAATA GAGA	2025
CEP94-A	.....C.....T.....	2025
D6948-A	.....T.....G.....	2025
TY89-A	.....	
Consensus	TGTCTGGAC GACGACATTA TGTGTGCA AGATCCATA CCTCTATTG TGGGAAACAG TGGAAATCTA GGCAT	2100
CEP94-A	.....T.....T.....T.....	2100
D6948-A	.....C.....C.....	2100
TY89-A	.....	
Consensus	AGCTTACATG GATGTGTTTC GACCCAAAGT CCGATCCAT GTGGCTATGA CCGGAGCCCT CAATGCTTCT GCGCA	2175
CEP94-A	.....A.....T.....T.....T.....	2175
D6948-A	.....C.....C.....C.....C.....	2175
TY89-A	.....	
Consensus	GATTGAGAA GTRAGCTTTA GAGACACAA GCTGCTACT GCACACGAC TTGGCTTAA GTTGCTGCTT CCGG	2250
CEP94-A	.....A.....T.....T.....	2250
D6948-A	.....C.....C.....C.....	2250
TY89-A	.....	
Consensus	WCATTTGAY GTTACACCG GTTCCACTG GGCACGCTT ATCAACGCTT TTTCTACAA TCGCGGAC TCGA	2325
CEP94-A	A.....C..T..A.....C.....A.....C.....	2325
D6948-A	T.....T..C..G.....T.....G.....T.....	2325
TY89-A	.....C.....C.....A.....	29
Consensus	CAGGTTWCT TACCTCAAC TWCCTATCT TCCACCAAW GCGGACGTC AGTWCATCT KGCCTTGGH GCCTC	2400
CEP94-A	...C..C..C.....A..A..C..T...C..AT..A.....C.....A..C..C..T...A...T..A..	2400
D6948-A	...C..C..T.....T..A..C..T...C..AT..A.....C.....A..G..C..G...A...C..T..	2400
TY89-A	...T..A..C.....T..C..T..C...A..CA..T...T...T..C..T..G...C...A...C..	104
Consensus	WGATTCAAA GAGACCCCG AGCTGATG TCTGTGAGW GCMATGAGW CWCWCGMA COTGAGCCA YRTT	2475
CEP94-A	A.....C.....GAG T..C..CA..A..A.....A..A..A..C.....C..A..	2475
D6948-A	A.....C.....GAG C..C..CA..A..C.....A..A..A..C.....G...C..G..	2475
TY89-A	C.....A.....AGA C..T..GC..T..A.....C..T..T..A.....C.....T..G..	179
Consensus	CCCTGCGC CTGCTGTCT TCACTGCTT GAGAGAAAY GGAATGTA CYGATATGC YAACTTGCN CTCAG	2550
CEP94-A	..AA..T..A...AGT..G.....C.....G..T.....G..T..C.....C.....A.....	2550
D6948-A	..AA..T..G...AGC..G.....C.....G..T.....G..T..F.....C.....A.....	2550
TY89-A	..GC..A..T...CAG..C.....T.....A..C.....A..C..C.....T.....C.....	254
Consensus	CGACCCGAC GGCATGGA TGTGATTT TCTGCAAY GCMCCGAG CCGGAGCA GTCCAGAG GCAA	2625
CEP94-A	.....C..TC.....CGA.....T..T.....C..A..A..A..A..C.....A..G.....	2625
D6948-A	.....C..TC.....CGC.....T..C.....C..A..A..A..A..C.....A..A.....	2625
TY89-A	.....A..CA.....AAA.....C..A.....T..T..C..G..C..A.....G..G.....	329
Consensus	GTATGGACR GCGGCTACG GATGGAGGC TGGGCGCCC ACCCGAGAG AGCAGACAG GGAAGAAGC ACAGC	2700
CEP94-A	...C..G..A..A.....TC..G.....A.....G..A.....A.....	2700
D6948-A	...C..G..A..A.....CC..G.....T.....G..A.....A.....	2700
TY89-A	...T..C..G..T.....TA..A.....G.....A..G.....G.....	404
Consensus	GATCTGAG AGATGARA CATGGGCAT CTACTTGA ACACCGAAT GGTAGCACT CAATGGCAC CAGG	2775
CEP94-A	.....A.....G..C.....T.....A.....T.....A.....	2775
D6948-A	.....A.....T.....T.....A.....T.....G.....	2775
TY89-A	.....C.....A..G.....C.....G.....C.....A.....	479
Consensus	GGACCGCCC GCGGCTTGA AGTACTGCA RAACACAGG GAAATACCG ARCCAGCA GGAATCTTA GACTA	2850
CEP94-A	G.....A.....G.....G.....G..C..A.....T..T.....	2850
D6948-A	G.....G.....G.....G.....T..T..A.....C..T.....	2850
TY89-A	C.....C.....A.....A.....A..C.....C..C.....	554
Consensus	YGTCAATGR GAGAAGGCC GGTGGCTCT AGAGAACAR RTCTTAAGG CAGCTACGTC GATCTACGG GCTCC	2925
CEP94-A	C.....T..A.....A.....A..C.....T.....	2925
D6948-A	C.....T..A.....A.....A..C.....T.....	2925
TY89-A	T.....C..G.....G..T.....C.....	629

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Fig.2a Contd. Alignment of IEDV A-segment cDNA sequences

Consensus	AGGACAGGCG GAGCCACCCC AAGCTTTCAT AGACGAAGTY GGCATGCTCT ATGAAATCAA CCATGCGGCT GTTC	3000
CEP94-A	.....A ..G..... ..T..... ..T....AA..... ..A... ..C..	3000
D6948-A	.....A ..G..... ..C..... ..C....AA..... ..G... ..C..	3000
TY89-A	.....T ..A..... ..C..... ..C....GG..... ..G... ..T..	704
Consensus	HAACAGAG CAGATGAAG ATCTCTCTT GACTGCGATG GAGATGAAGC ATGCAATCC CAGCGCGCT CTAC	3075
CEP94-A	A....A..A .....A. .T.....T. ......... ..T...	3075
D6948-A	C....A..A .....A. .T.....C. ......... ..C...	3075
TY89-A	A....G..G .....G. .C.....C. ......... ..C...	779
Consensus	AAAGCCGAG CCAAAACCA ATCTCTCNC ACAGAGCCC CCTGACGCG TGGGCGCTG GATCAGGCG GTCTC	3150
CEP94-A	.....C..... ..A..... ..T..... ..A.C .....	3150
D6948-A	.....C..... ..A..... ..T..... ..G.F .....	3150
TY89-A	.....A..... ..T..... ..A..... ..A.G .....	854
Consensus	TGATGAGGAC YTGAGTGAG GTWCTGGGA GTCTCCGAC ACCACCGCG CAGGTGTGA CACCAATTTC KBBT	3225
CEP94-A	...T..... C.T..... .TA..... ..T..... ..CG GACT.	3225
D6948-A	...T..... C.T..... .CT..... ..C..... ..CG GCGA.	3225
TY89-A	...C..... T.G..... .CT..... ..T..... ..AA TCAC.	929
Consensus	AGAGGATTC AAATTGGATC CTTTGGCGG TCCCC	3260
CEP94-A	.CAC..C.C .....	3260
D6948-A	.CAC..C.C .....	3260
TY89-A	.GTG...T.G .....	964

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Fig.2b

Alignment of IBDV B-segment cDNA sequences

Consensus	GGATACGATG GGTCTGACCC TCTGGAGTC ACTAAATAC GTGGCTACTA GGGGTGATTA CCGGCGCTG CTGCC	75
CEP94-B	.....C...AA ..G.....G. ....	75
D6948-B	.....T...GC ..A.....A. ....	75
Consensus	ACGTTAGTG CTCTCTTCT TGTATGTTCT ECGACGATGA GTGACTTTT CAATAGTCCA CAGGCGGAA GCAGG	150
CEP94-B	.....G..... ..A..... ..C..... ..C. ....	150
D6948-B	.....A..... ..G..... ..T..... ..A. ....	150
Consensus	ATHTCAGCAG GGTTCGGCAT AAGGCTACH GCTGACGAG AYTGAGAGA ACTCTGATC CCTGAGTTT GGGTG	225
CEP94-B	..C..... ..T..... ..A. ..C..... ..T..... ..A..T. ....	225
D6948-B	..A..... ..A..... ..G. ..T..... ..C..... ..G..C. ....	225
Consensus	CCACCTGAGG ATCCCTTTC CAGCCTTMT COMCTGCGA AGTTCTCTAG GGAAGACGGC TACAATTTT TCCAG	300
CEP94-B	.....GC..T. .... ..A.....A. .... ..A..G..... ..AG..T. ....	300
D6948-B	.....CT..G. .... ..T.....C. .... ..G..A..... ..GA..C. ....	300
Consensus	CCACGCTTC TCCCTGAGAA TGAGGATAT GAGACGATC AATATCTCC GACTTENGCH TGATGEMRC AGATA	375
CEP94-B	.....G..C..... ..C..... ..A...T..... ..C.A. ....	375
D6948-B	.....A..T..... ..T..... ..T...C..... ..A.G. ....	375
Consensus	GAGGCGCTG TTATAAACC NACTCTACT CTCCCTATG GAGATCAGA GTACTTCCH AAREACTAC CAACA	450
CEP94-B	..A..G.... ..C..T..... ..T..... ..T..... ..A..G..... ..G.....	450
D6948-B	..G..A.... ..A..C..... ..C..... ..C..... ..T..... ..A.....	450
Consensus	CATCGGCCA GCAAGGAAA GCGCAATGG TACCCACCG AYATGCAAT ACTCAGCAG ATGTTTACT TTTT	525
CEP94-B	..T.....T. .... ..G.. ..A. ..C.....C. .... ..T...C. ....	525
D6948-B	..C.....G. .... ..A. .... ..C. ..T.....T. .... ..C...T. ....	525
Consensus	CTCCGCTTC CAGAGGCCA NGAATGCTT AAGATGAG TACCCCTTT TACCCAAAC ATGAGGATA ARGC	600
CEP94-B	.....A.....A ..C..GG. ..A ..G.....A. ..A.....CT. G..... ..A..G..C. ..G...	600
D6948-B	.....C.....C A..TAA...T ..A.....G. ..C.....AC. A..... ..T..A..T. ..A...	600
Consensus	TATGAGTGT GAGCTTACT GAGACGAGN ACTGACTTG TGTATGAA GAGGTTTGC ACTGAGAA ACCCA	675
CEP94-B	..T..A.... ..A..A ..TC..... ..G..C..... ..G.....C..... ..A.....	675
D6948-B	..C..G.... ..G..C ..CA..... ..T..T..... ..A.....T..... ..G.....	675
Consensus	AACAGATC CTCTAAGCT TGGTACACT TTGAGACA TGGCCAGCT ACTTGACATC ACHTACCG TAGCC	750
CEP94-B	.....G.... ..T..... ..C..G..... ..AC..... ..G.....	750
D6948-B	.....A..... ..C..... ..A..C..... ..T..... ..G.....	750
Consensus	CCACCGGCT AGATGACAA GCGCTGGTA CCACTACAA GGTGGGCTC AAGGATGTT GTACGACCG GAGAC	825
CEP94-B	.....G..... ..A..... ..C..... ..A..... ..A...	825
D6948-B	.....A..... ..G..... ..A..... ..T..... ..C...	825
Consensus	GTAGTGGG AMTTGAGT TGAGATAC CTCCCAAA TCACCTCA GTCATCAAT GACTTCCT ATGT	900
CEP94-B	.....C. ..C..... ..A..T..... ..A..... ..A..A. ....	900
D6948-B	.....G. ..A..... ..G..C.... ..G..... ..G..C. ....	900
Consensus	GCTGACCA AAGGAGAC NATTGGGAG ATGATAGTA TTTTCAACA GTTCTTGA GAGCTATCA CACTG	975
CEP94-B	.....G..A.....C..... ..T..C..A..... ..CA..... ..A..A...	975
D6948-B	.....A. ..T.....G.... ..C. ..A..G..... ..TC..... ..G..G...	975
Consensus	YTGAGCAG GTCCAGGAC AAGGCTCA AACAGAGA AGCTCTCAG CATGTAAAT GACTATGAT ACTA	1050
CEP94-B	T.....A..... ..G.....A..... ..A..... ..T..... ..T.....	1050
D6948-B	C.....G..... ..A.....G..... ..G..... ..C..... ..C.....	1050
Consensus	TCTGTGGC TTGTGTTTC NAGGCTGAG AGGTAGACA AAGTACATG GTCACCAAG ACCCGGACA TATG	1125
CEP94-B	.....C..... ..A.....A..... ..T..... ..G..... ..G.....	1125
D6948-B	.....T..... ..C.....G..... ..C..... ..C..... ..T.....	1125
Consensus	TGACTCCAT CCGCAACAA CCTCATGAT TGTATGATA CCGGCGGCT GATGTCAAT AGCCCAAYA AGTG	1200
CEP94-B	.....C..... ..T.....C..... ..C..... ..T..... ..T.....	1200
D6948-B	.....A..... ..A.....A..... ..T..... ..T..... ..C.....	1200

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Fig.2b Contd. Alignment of IBV B-segment cDNA sequences

Consensus	TTCACATTC ARGGGTGTCC TTCACCTTAC AATTCACCC GGTTCAGAGG WGGGTTTAAAC AGGTCCTGAG AGTGG	1275
CEP94-B	..... A..... A..... ..A..... ..C..... A...T.G... ..C.....	1275
D6948-B	..... G..... G..... ..G..... ..T..... T...C.A... ..G.....	1275
Consensus	ATATGTCCTC CCGAGAACC CAGGCTTTC GTATCTCCAG ACACATATA CATTTCTTAC TCGACACCT GGTAC	1350
CEP94-B	...T...C... ..A..... ..TC.T... ..G..... ..C..... ..A.....	1350
D6948-B	...A...T... ..T..... ..CT.A... ..T..... ..T..... ..C.....	1350
Consensus	TCAATTCACC TAGAGAAGGG TGGGCAAC TCACACCTTC AACACATCCA RCGGCGATG TACTACATTC TTAAC	1425
CEP94-B	..... ..F..C... ..A.....A... ..A.....C...	1425
D6948-B	..... ..G..T... ..G.....C... ..T.....	1425
Consensus	ACAGGTGCT CAGAYAACGG TGAACCATG TTCAATCACA CATGGGCCAC CTTCGCGATG AACATGGCCC CAGCT	1500
CEP94-B	....G.... .A..C.... C....A... ..A..... ..C..... ..T....	1500
D6948-B	....A.... .C..T.... T....C... ..G..... ..G..... ..A....	1500
Consensus	CTAGTCTGTC ACTATCTCTG TCTGATWATG AACCTTCACA TTAAGACMTA TGGTCAAGGC AGTGGGATG CAGCC	1575
CEP94-B	....G.... ..G.... C....A... ..G..A... .T....C... ..C.....	1575
D6948-B	....T.... ..A.... T....T... ..T..G... .C....A... ..T.....	1575
Consensus	ACCTTCATCA ACAACCACTT TTGAGCAGS CTGTGCTTGG ACCAGTGGAA CTTCATGATG CAGCTTACGC CAGAC	1650
CEP94-B	..G..... ..C.... CT.G....G ..A....T... ..C.....GA ..G..C..A... ..	1650
D6948-B	..C..... ..T.... TC.T....C ..T....A... ..T.....AG ..A..T..T... ..	1650
Consensus	AGCGAGAT TCAATCAAT TGAGACAG CTRGATCA ACTTAAAT TGAGAGTCC ATTGATATA TTAGG	1725
CEP94-B	....G.... ..A..... ..G..... ..A..T... ..T..... ..T....C...	1725
D6948-B	....A.... ..G..... ..A..... ..G..C.... ..C..... ..C....T....	1725
Consensus	GGCAAGCTCA GACAGCTTGT CCTCTTCCA CACCAAGGCT ACCTGATGG RGGGTTGAA CCGAGCAAT CAGC	1800
CEP94-B	.....G... ..T..... ..G..... ..G....T... ..A...T....	1800
D6948-B	.....C... ..C..... ..A..... ..A....C... ..G...C....	1800
Consensus	CCACTGTGG AGCTGACCT ACTGGGTGG TGGGACAT ACAGCAAGA TCTTGGGATC TATGTGCGGG TGCTT	1875
CEP94-B	.....T... ..T..... ..A..G... ..A..T..A... ..C..... ..C.....	1875
D6948-B	.....A... ..G..... ..C..A... ..T..A..T... ..T..... ..T.....	1875
Consensus	GACAAGGAC GCTATTTTTC TTCTGCTGG TATCCCAAG GATAGAGAA YAAAGATCTC AATCCAAAG TTGGG	1950
CEP94-B	.....C..... T..... ..G....A..... C..G..T... ..G....A...C...	1950
D6948-B	.....T..... C..... ..A..... ..G..... ..T..A..C... ..A....G...T...	1950
Consensus	ATGAGCAG CATAAAGT WTCAGATAY GAGGCTTGA GGTGGZAGG TGGTGGAC TACCACTCC TGAAC	2025
CEP94-B	.....G.... ..G.... A.....T... ..C..... ..C..... ..C.....	2025
D6948-B	.....A.... ..A.... T.....C... ..C..... ..C..... ..C.....	2025
Consensus	AAAGCTTCCA AGAAYATGC ARGTCCTCT CCGGCGATC TGAAGGCCAA GGGGTTCCCT CTCATGATGT TCTT	2100
CEP94-B	....C.... ..T..C... ..G..C..C... ..C..... ..A....C.... ..A....	2100
D6948-B	....T.... ..C..T... ..A..T..A... ..C..... ..A....T.... ..C....	2100
Consensus	GGGATGCT CAGATGCTC HZAGTTCGG GAGCTTTCG AAGCTTCAA TATCAGCTG ACATGATAY CAGAG	2175
CEP94-B	.....T...C.... A.....T... ..G..C.... ..C..... ..C..... ..T....	2175
D6948-B	.....A...T.... C.....A... ..A..T.... ..C..... ..A....C... ..G....	2175
Consensus	AGCTTGGCC AACTAACAR RCGATACCC CCCAARCTTC CAAATGTCAA CAGACCAATC AACATGCGG GACTT	2250
CEP94-B	....A.... ..G....A G..... ..G..C.... ..C..... ..T..G... ..A..C...	2250
D6948-B	....C.... ..T....G A..... ..A..T.... ..C..... ..C..T... ..G..A...	2250
Consensus	AAGGAGTCA GCAATGCCCT CAGACCGGT CGGTAYAGRA ATGAGCGCG ACTGATGAT CTGCTCTTTC TAGCC	2325
CEP94-B	.....C..... ..T....C..G... ..C..... ..G....T... ..T.....	2325
D6948-B	.....T..... ..C..... ..T..A... ..T..... ..A....C... ..C.....	2325
Consensus	ACGCGHGA GCGGCTCA NGATGATGY AAGGCCAAG CAGAGCGGA GAATCTCAC AATCTYAGC CAGAT	2400
CEP94-B	..A..AA.A... ..T..G... ..A..T....T... ..A..... ..C..... ..A..C...	2400
D6948-B	..C..CC.C... ..A..A... ..G..C....C... ..G..... ..T..... ..C..T...	2400

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Fig.2b Contd. Alignment of IBV B-segment cDNA sequences

Consensus	GACCCGATG CAGACTGCTT TGAAGTCA GAACTCTCT CAGACTCTCT GAGAAAGCC GACCTTCCA GCAAG	2475
CEP94-B	..... C...A.A... ..T... ..T... ..C... ..	2475
D6948-B	..... T...C.G... ..C... ..G... ..T... ..	2475
Consensus	GTCGCTCACT CAGACTCTCT GAGAAAGCC GAGCTCTCTG AAGCTGTCA GTCGCTCTCT GTGCTACTC CCAAG	2550
CEP94-B	.....C... ..C... ..A..T.. ..G..T..C ..T... ..C... ..	2550
D6948-B	.....T... ..T... ..G..C.. ..A..C..A ..C... ..A... ..	2550
Consensus	TACCCAGAG TYAAGAACCC ACAGACGCC TCCAGCCCG TTGTTGGCT CCAGCTGCC GCGAGAGAG CCACC	2625
CEP94-B	.....A. .C..... ..A..... ..A..... ..	2625
D6948-B	.....G. .T..... ..G..... ..G..... ..	2625
Consensus	GCTGTCAGG CAGCTCTCT CAGAGAGAG AGAGCAGAC CAATGGGAT GAGGCTCCA ACAGCTCCA AGAAC	2700
CEP94-B	.....C..... ..A..... ..C..... ..	2700
D6948-B	.....A..... ..G..... ..T..... ..	2700
Consensus	GCCGTGAAA TGGCCAAAG GCGGCACTC CAAAGAGA GCGGCCAAT GCCATGTGG GAGCACTCA AGAG	2775
CEP94-B	.....C..... ..G..... ..C..... ..	2775
D6948-B	.....A..... ..A..... ..T..... ..	2775
Consensus	AGGACTAA TCCAGAGCC GGTATCCCG GCTTGGCT GCGGGGCCC CC	2827
CEP94-B	.....T..... ..	2827
D6948-B	.....C..... ..	2827



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Fig.3a IBV polyprotein alignment

Consensus	HTMLQDOTQQ IUVFIRSLIM PTTPASIPD DTLKQTLAS ETSTMLAVQ DTGSLIVTF PGFPGSIVGA HTLQ	75
CEP94-PP	.....	75
D6948-PP	.....	75
TY89-PP	.....	
Consensus	SNQYKPDQM LLAQHLFAS YNYCLVRS LTVRSSTLPG GVTALQSTIR AVTFQGSLSL LTVSTINGLM SMEM	150
CEP94-PP	.....	150
D6948-PP	.....	150
TY89-PP	.....	
Consensus	INDKIGNVLV GEGVTLSLP TSTLQTVEL GDPFPAIGLD PKQVATCDSS DRPVYTIYA ADOTFESQY Q.GGV	225
CEP94-PP	.....	225
D6948-PP	.....	225
TY89-PP	.....	
Consensus	TITLPSASID AITELSGOE LWTQTSV.GL LGATITILIG PDOTAVITRA VAA.HSLT.G TDEL.FPN.V IPT.E	300
CEP94-PP	.....V.....H.....V.....N.....T.....L.....L.....N.....	300
D6948-PP	.....I.....Q.....I.....D.....A.....M.....I.....S.....	300
TY89-PP	.....	
Consensus	ITQPIYSIKL KIVTSKSGQQ AGDQMSMA. GSLAVTINGQ NYGALRPVT LVAYERVATO SVTVAGVEN FELIP	375
CEP94-PP	.....R.....	375
D6948-PP	.....S.....	375
TY89-PP	.....	
Consensus	NPFLAQLVY EYGFDPQAM HTYLILSER DRIGIKTVWF TRSTIDFKEY FMEVADLMSF LAINGAGGFK DIIRA	450
CEP94-PP	.....	450
D6948-PP	.....	450
TY89-PP	.....	
Consensus	.KRIAVPVVS TLPTTAAPLA HAIGGVDTL LGDEAQAASQ TAAASQEAR AASGRIRGLT LAANGGVYEV ANLQ	525
CEP94-PP	I.....	525
D6948-PP	L.....	525
TY89-PP	.....	
Consensus	VPGPVVDGI LASFG.LGA HMLCVLRQ ATLPFVVITV VEDANTKAL HSKMFVING VRELQPPSQ RGSYI	600
CEP94-PP	.....V.....	600
D6948-PP	.....I.....	600
TY89-PP	.....	
Consensus	RTLSGRVYQ YAPQGVLSL TQDITTVST DEVMQDSIML SKDPFPIVIG HSCMLAIYM DVFRKVPIN VAMTG	675
CEP94-PP	.....	675
D6948-PP	.....	675
TY89-PP	.....	
Consensus	ALAA.GEIR. VSFSTELAT ANKLGKLAG PGAFDVWTO. HQTTFIKRFP HMPEDWQLF YLMLPLFPN AGROY	750
CEP94-PP	....C....K.....F.....	750
D6948-PP	....Y....N.....S.....	750
TY89-PP	.....T....P.....	28
Consensus	HLAQAASEFK RYFLESAVA AMEAAANVDP LPQSALSVTM VLEKSGIVTD MANVALSDW AMQSGUPLAN APQAG	825
CEP94-PP	.....	825
D6948-PP	D.....	825
TY89-PP	...L.....D.....D.....R...Q...K.....	103
Consensus	SKSQRAKYGT AGYQVEARGF TPKEAQREK TRISKKESTM GIYFATPBNV ALNGHGPSP QQLKYNQWR EIPDF	900
CEP94-PP	.....	900
D6948-PP	.....	900
TY89-PP	.....E.....	178
Consensus	NEDYLDYVHA EKERLASSEQ ILRANTSIG APQARPPQA FIDEVAKVYE IMKROPKQZ QMKLLATAM EKKER	975
CEP94-PP	.....	975
D6948-PP	.....	975
TY89-PP	...F.....V.....R.....	253
Consensus	NFRAPPKPK PKNAPTORF PQLGHWIRT VEDDLK	1012
CEP94-PP	....L.....	1012
D6948-PP	.....A.....	1012
TY89-PP	.....S.....	290

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### Fig.3b IBDV VP1 alignment

Consensus	MSD.FMSQA RS.IGAAPGI KPEAGQDVE LLIFKVVVF EDPLASTVRL AKFLAKMTE .LQFRLPFI EHYET	75
CEP94-VP1	...I.....T.....V.....	75
D6948-VP1	...V.....K.....I.....	75
Consensus	DQILPDLANI RQISGAVLKP TSLPFDQDS YPFKYTPTR PSKEKFWAYF PDIALLEQNI TLFLQVFA. ...LAD	150
CEP94-VP1	.....N..E...	150
D6948-VP1	.....T..E...	150
Consensus	EVTLLTQNIK DKAYGQTYM QGATKLVAKK EVATGRWPK DFLGLQTYR SLAQIDITL PVGPFQEDK FNVFL	225
CEP94-VP1	.....	225
D6948-VP1	.....	225
Consensus	TKVFERNLV TGVVDG.FEV EYLPKIKLK EESGLPTVGR TQSTIGENI AISKQFLAKL S.LLQQAQT KQNK	300
CEP94-VP1	.....D.....T.....	300
D6948-VP1	.....E.....A.....	300
Consensus	EKLLESLDY WYLSQGLLP KARYDKSTW LKSTYNIWA PSPHLEKLE ITWFWESFP EYVLENGCT SLYCP	375
CEP94-VP1	.....	375
D6948-VP1	.....	375
Consensus	HPFQGLKEI VEMI.AP.EF KALVADNIT IVHENTWYSI DLKQENCT RQHQQAATY ILTQKMDG DPWF	450
CEP94-VP1	.....L..E.....	450
D6948-VP1	.....N..D.....	450
Consensus	QTWTFARKI APALVDESC LDEHQLKTY QGEGQAATY DSHLLSTLV LQQLKLM.QP .PQSEVKEI EKKLG	525
CEP94-VP1	.....R..E.....	525
D6948-VP1	.....K..S.....	525
Consensus	INPIERSID DIERKLQLV .LAQTOYLG QVEPEQ.SPT VELDGLMKA TTKULQITV FVLDKELFC SAAYP	600
CEP94-VP1	.....L.....S.....	600
D6948-VP1	.....P.....P.....	600
Consensus	KGVKSKLS KVICQATKV VYEAELVVG GNTYPLNKA CYMA.AAKR HLEAGTFLD EYLAHSLK EYQEA	675
CEP94-VP1	.....G.....	675
D6948-VP1	.....S.....	675
Consensus	FQPMILTV T.ESLAKLS. PVPPKPPVVM RFWVTOGLA VSHALQTRY KIRAGLSLV LIATARSLO DAVKA	750
CEP94-VP1	.....S.....K.....	750
D6948-VP1	.....P.....R.....	750
Consensus	KAAKILKKS KPDDPDAMP ERSETLSLL EKADIASKVA HSAVETSDA LEAVQSTVY TNYPEVONP QTASH	825
CEP94-VP1	.....	825
D6948-VP1	.....	825
Consensus	FVGRHLPAK RATGVQALL GAGTERPKK EAPTSKNAV KQAKKQKQK ESRQ..	881
CEP94-VP1	.....QF	881
D6948-VP1	.....	879

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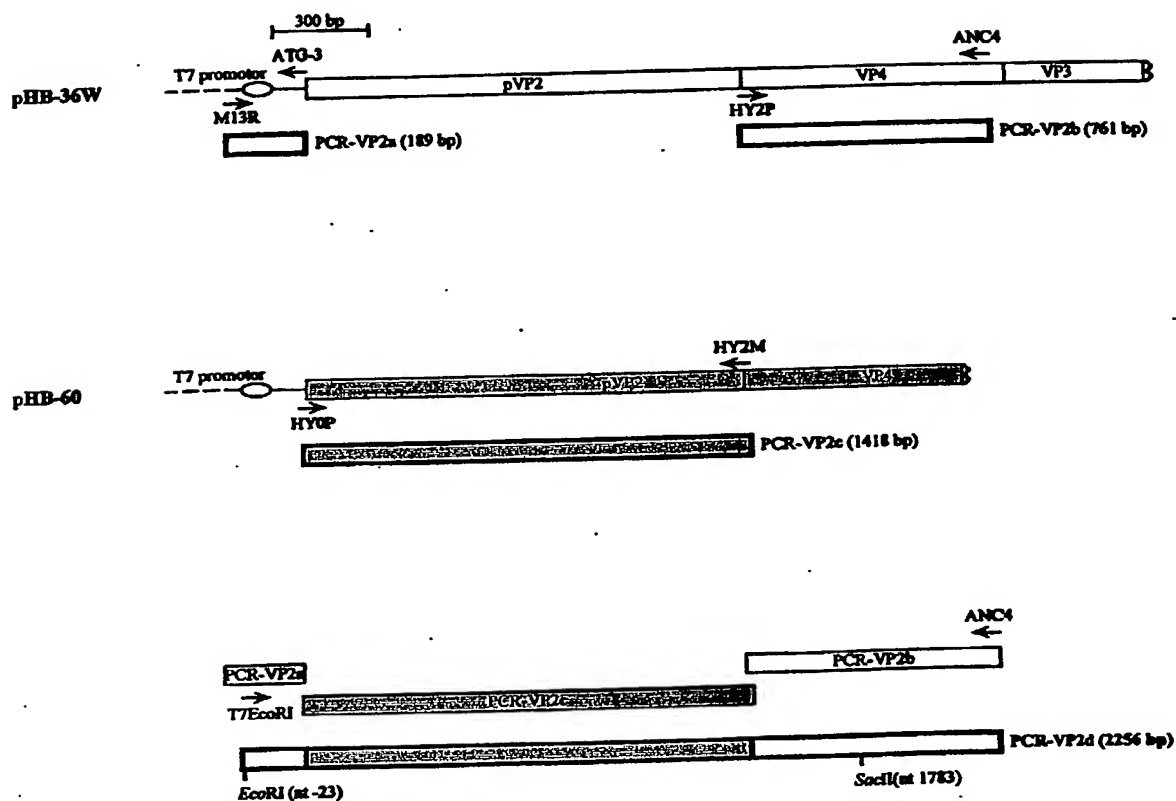
Fig. 3c IBDV VP5 alignment.

Consensus	MVSRDQTNDR SDD.PARSHF TDCSVHTFSS DANRRTGVHS GRHP.EARSQ	50
D6948-VP5	.....E.....R.....	50
CEF94-VP5	.....K.....G.....	50
Consensus	VRDLQLQFDC GGRVRANCL FFW.FWLNCG CSLHFAQWE LQVRSDAPDC	100
D6948-VP5	.....F.....	100
CEF94-VP5	.....I.....	100
Consensus	FEPTQLQLL QASESESRSE VIGT.WWRLC TK.HHGRUHL FKKPE	145
D6948-VP5	.....F.....M.....	145
CEF94-VP5	.....S.....R.....	145



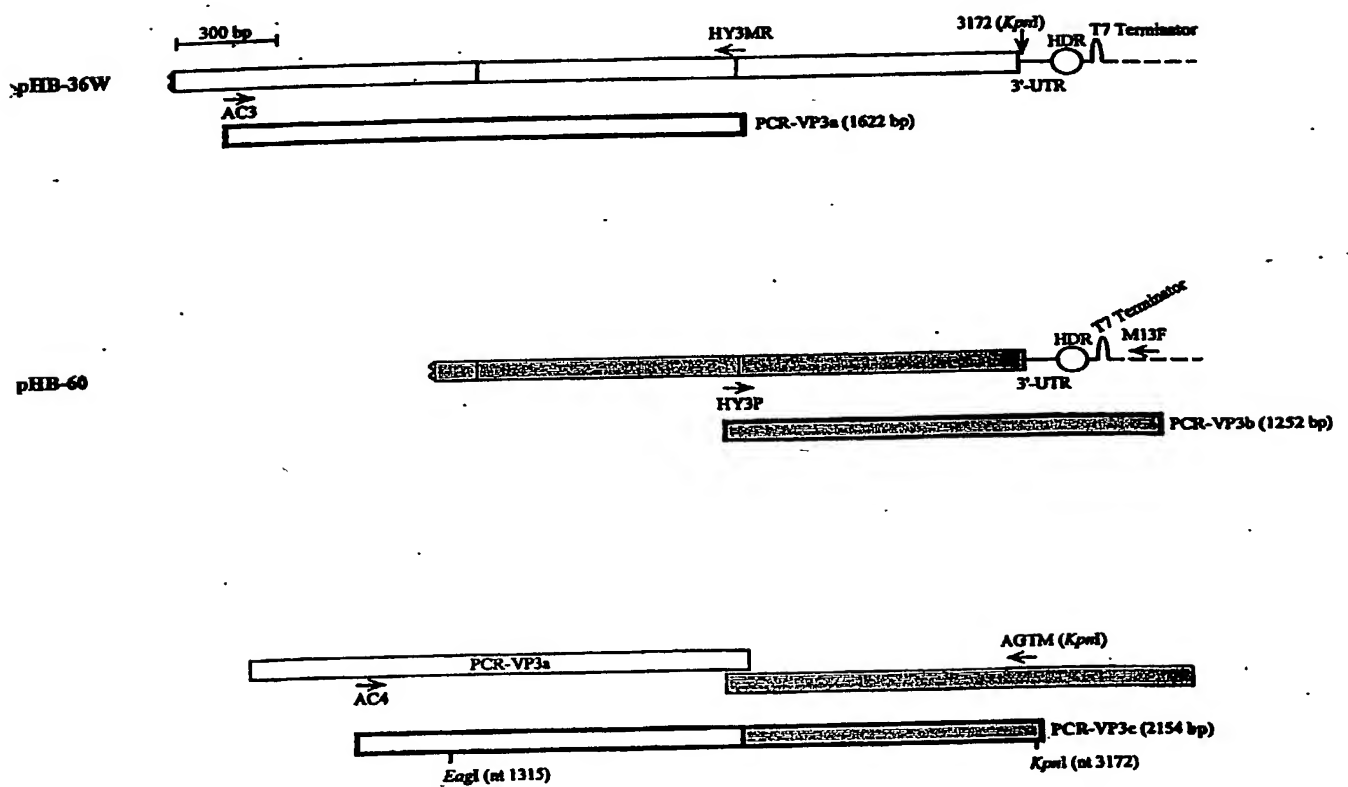
**Fig. 5a**

Schematic representation of the construction of PCR fragment PCR-VP2d



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**Fig. 5b** Schematic representation of the construction of PCR fragment PCR-VP3c

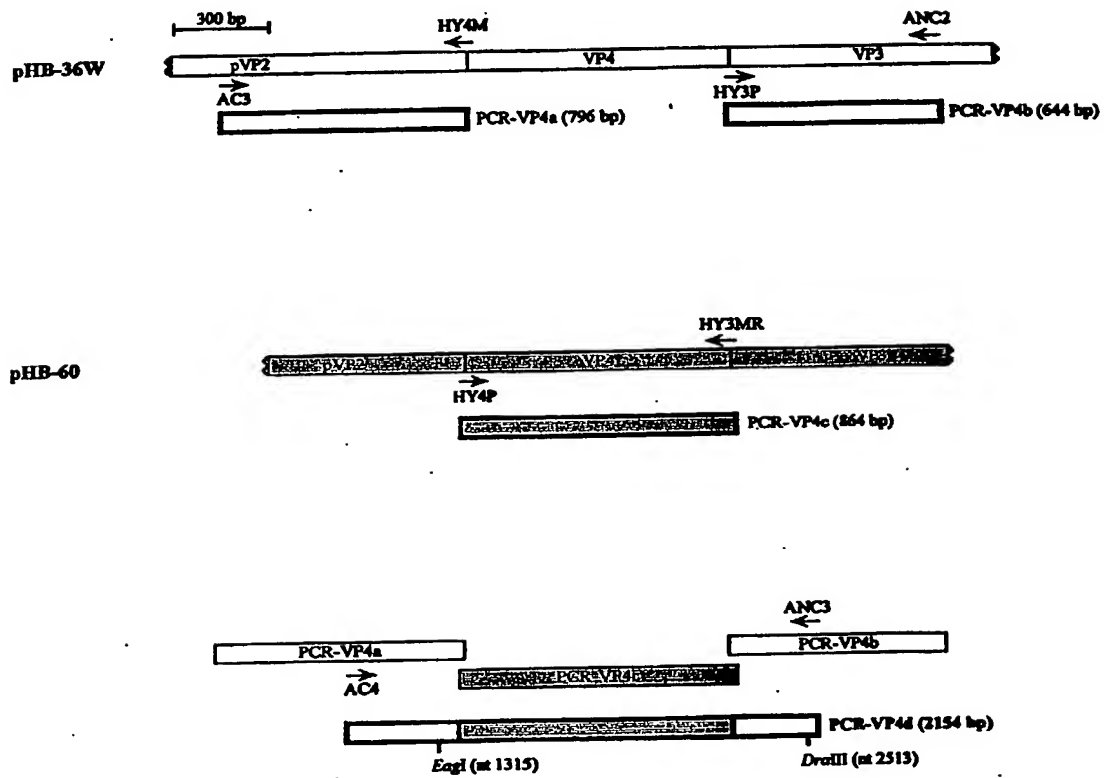


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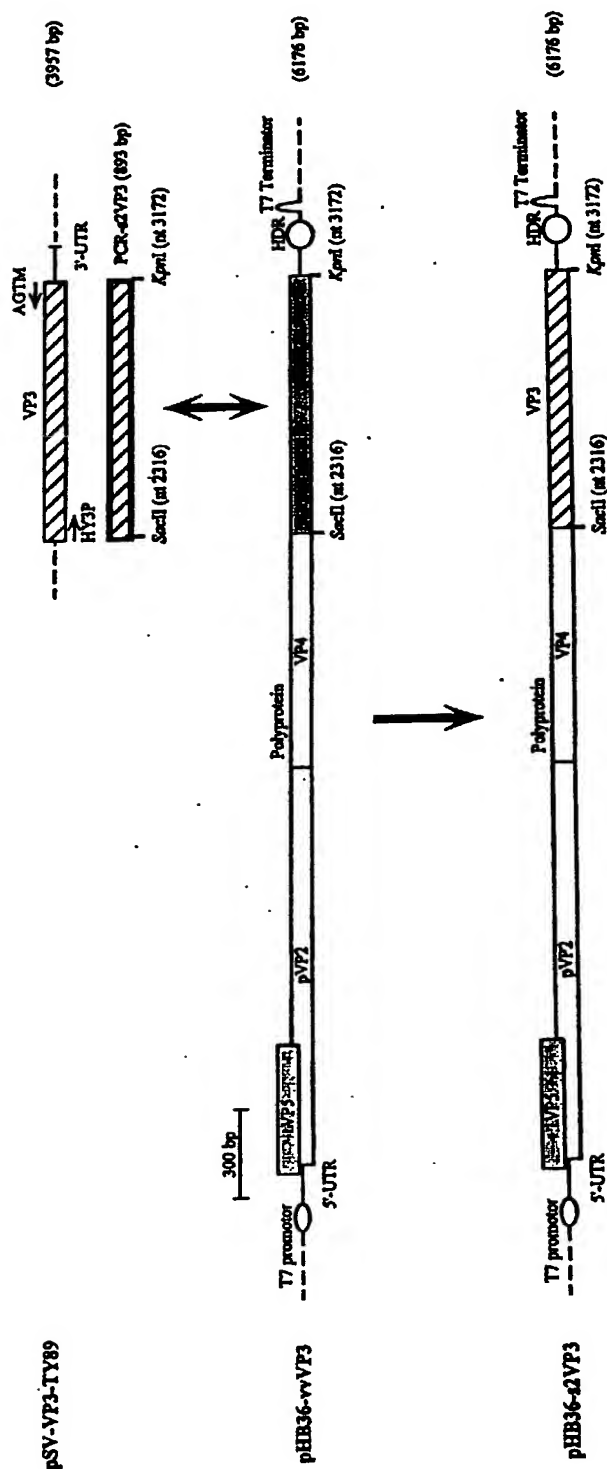
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**Fig. 5c**

Schematic representation of the construction of PCR fragment PCR-VP4d



**Fig. 5d** Schematic representation of the construction of plasmid pHB36- $\alpha$ VP3





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Fig. 5e Schematic representation of the construction of plasmid pHB36-ΔVP3C

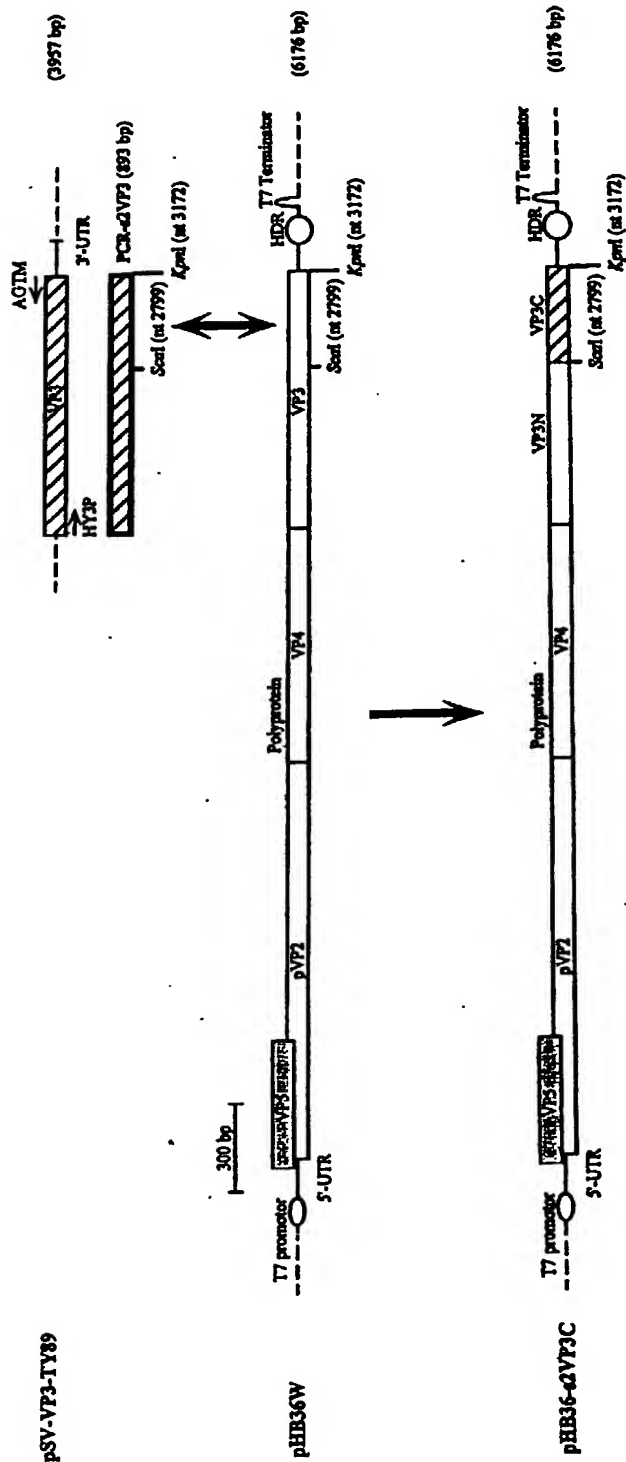
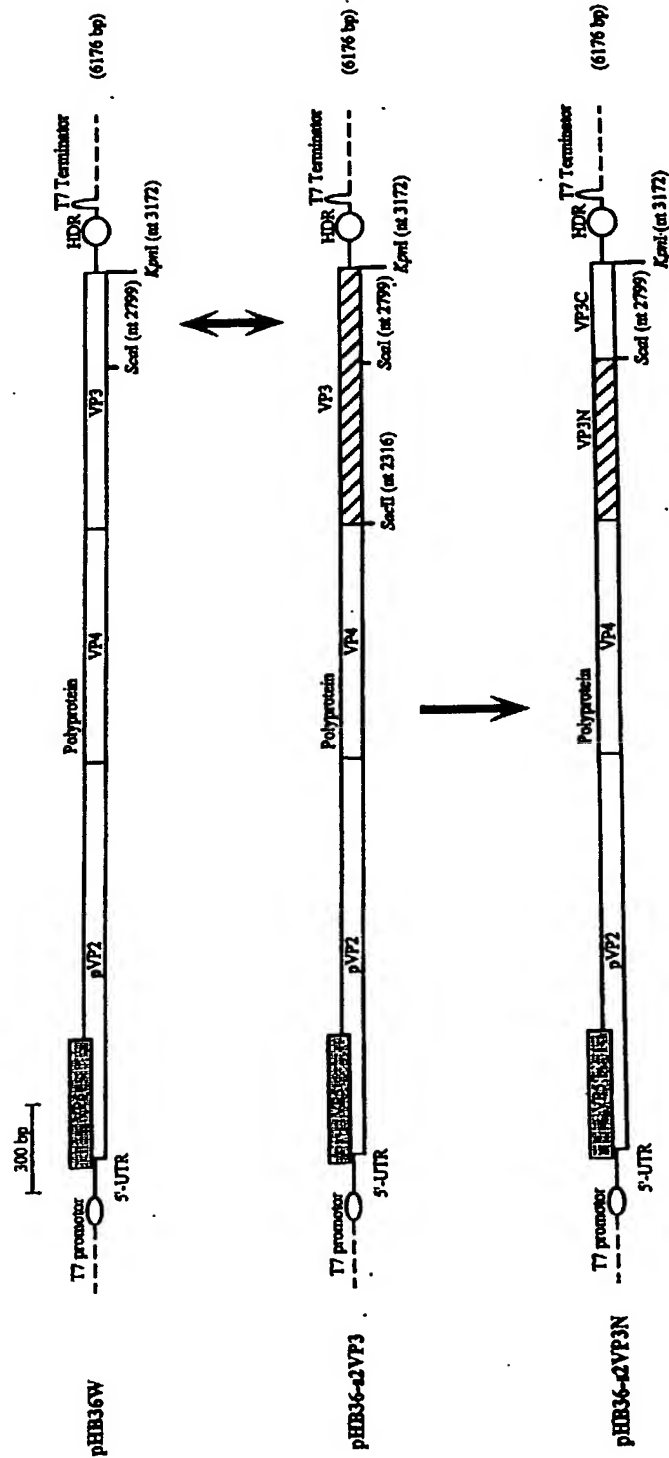
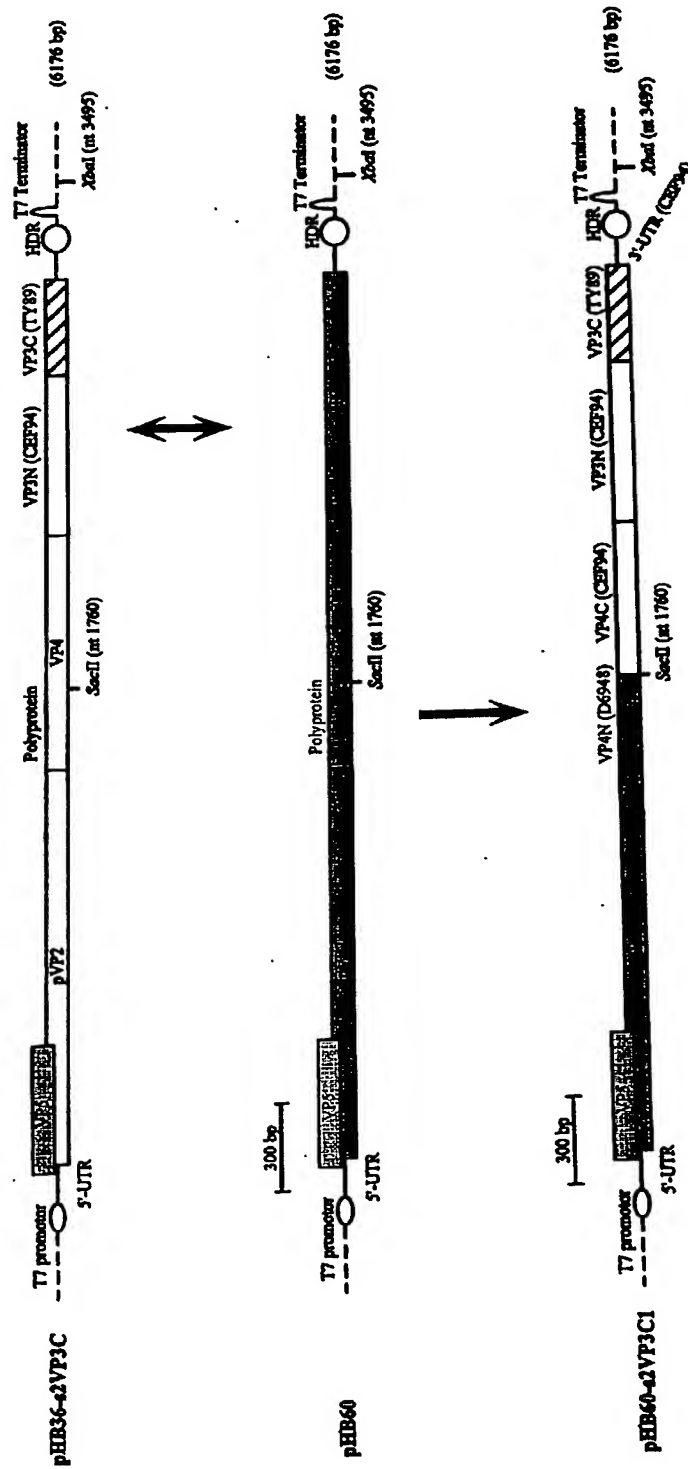


Fig. 5f Schematic representation of the construction of plasmid pHB36-Δ2VP3N



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Fig. 5g Schematic representation of the construction of plasmid pHB60-Δ2VP3C1



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Fig. 6

CEF94-PP TY89-PP	<p>VP4 ← ———→ VP3</p> <p>↙ SacII</p>	724-FPHNPRD WDRLLPYLNLP YLPPNAGRQY HLAHAASEFK ETPELESAVR AMEAAANVDP LFQSALSVFM WLEENGIVTD 800
		724-.....T.....F...L.....D....D....R...Q... ..800
CEF94-PP TY89-PP	<p>↙ Scal</p>	MANFALSDPN AHRMRNPLAN APOAGSKSOR AKYGTAGYGV EARGPTPEEA QREKDTTRISK KMETMGIYFA TPEWVALNGH 880
		.....K..... .. .. .. ..880
CEF94-PP TY89-PP		RGPSPGQLKY WQNTREIPDP NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APOGAEPPQA FIDEVAKVYE INHGRGPNQE 960
		.....E.....P..... ..V..... ..R... ..960
CEF94-PP TY89-PP		QMKDILLITAM EMKERNPRA LPKPKPKFNA PTQRPGRGLG RWIRTVDDE LB 1012
		.....P.....S..... .. ..1012

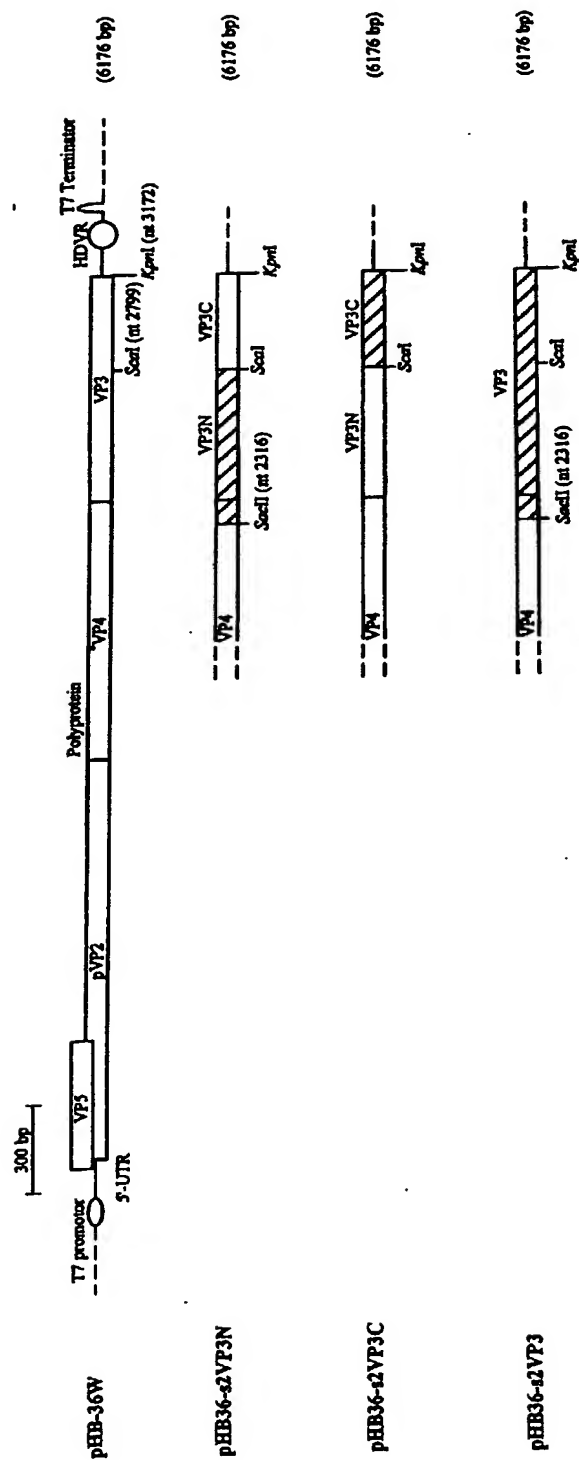


Fig. 7

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Fig. 8C

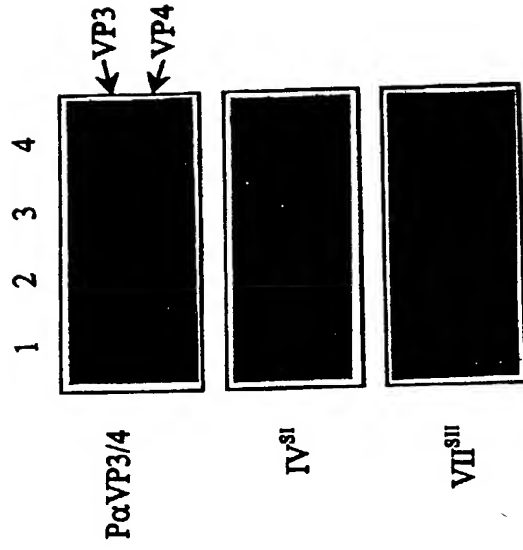


Fig. 8B

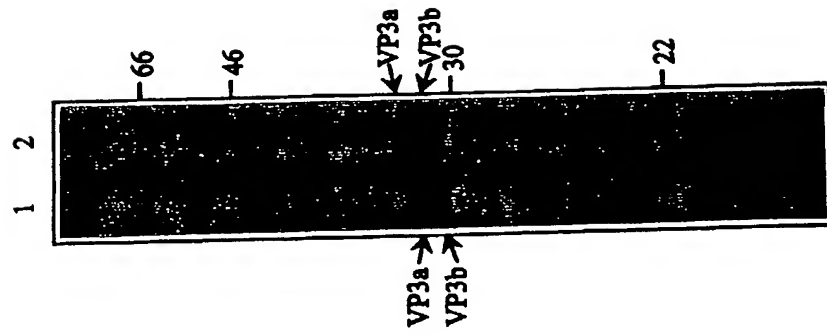
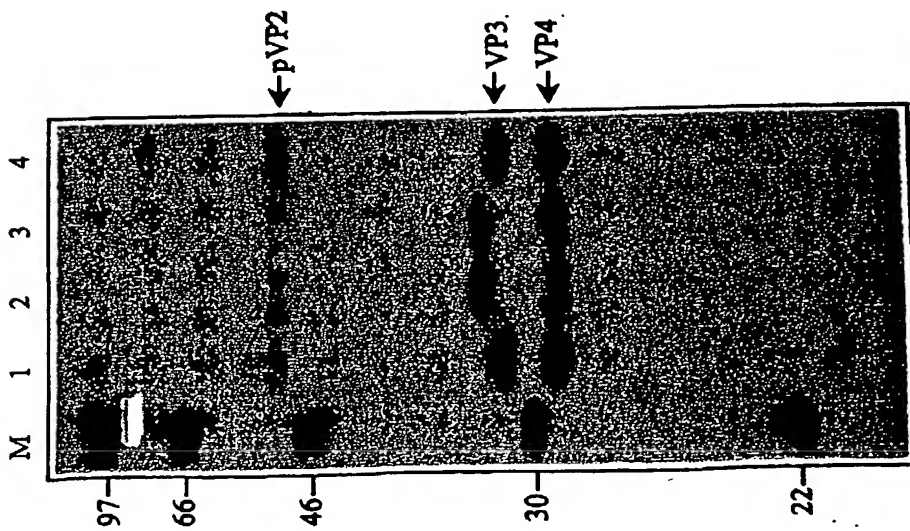


Fig. 8A



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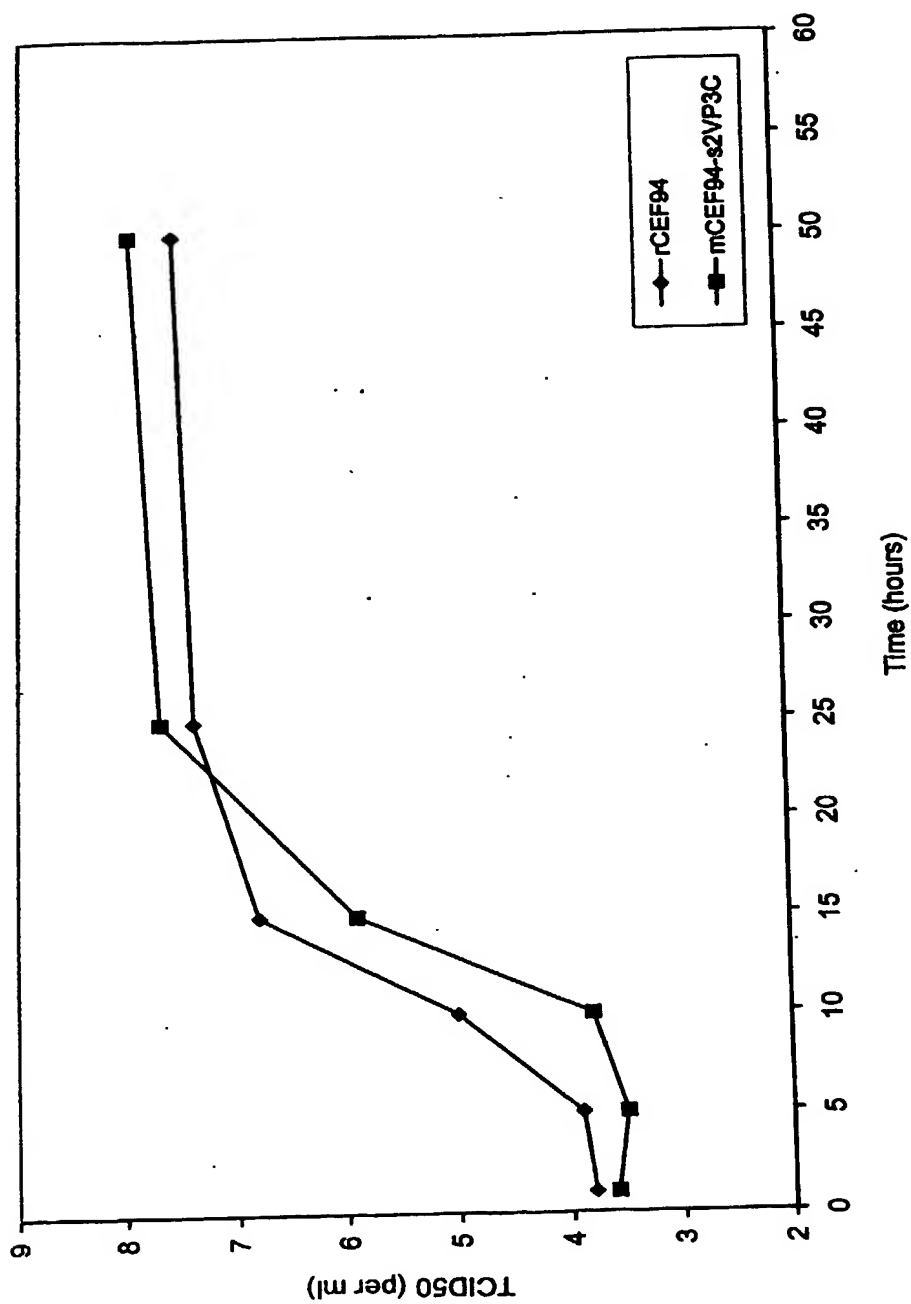
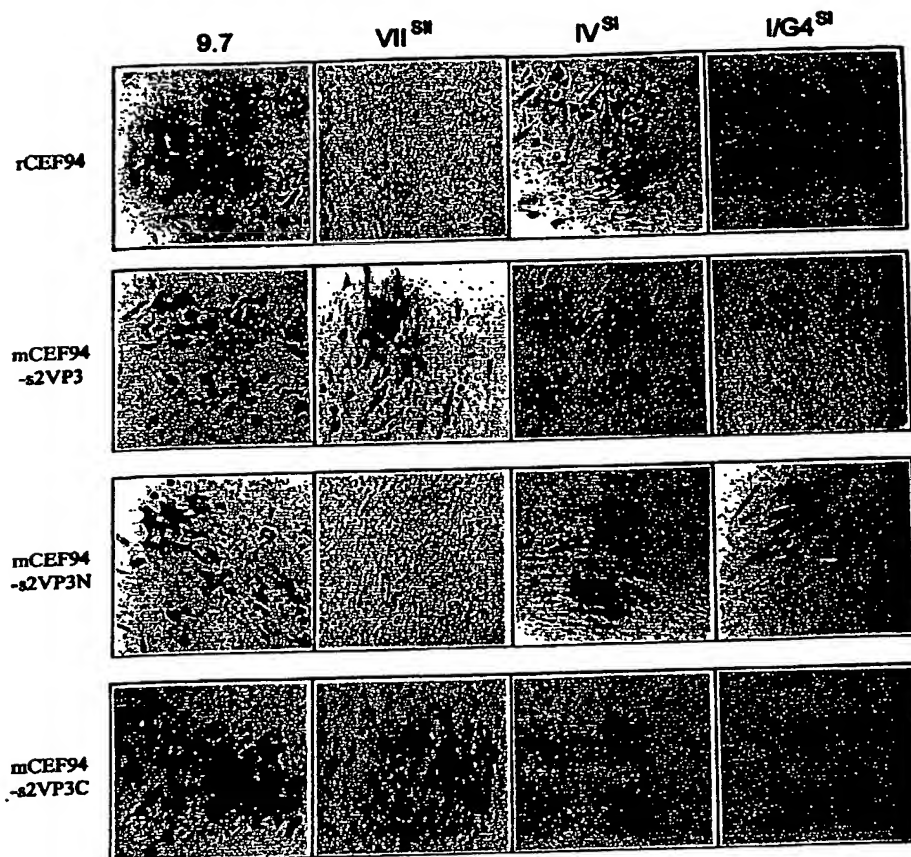


Fig. 9

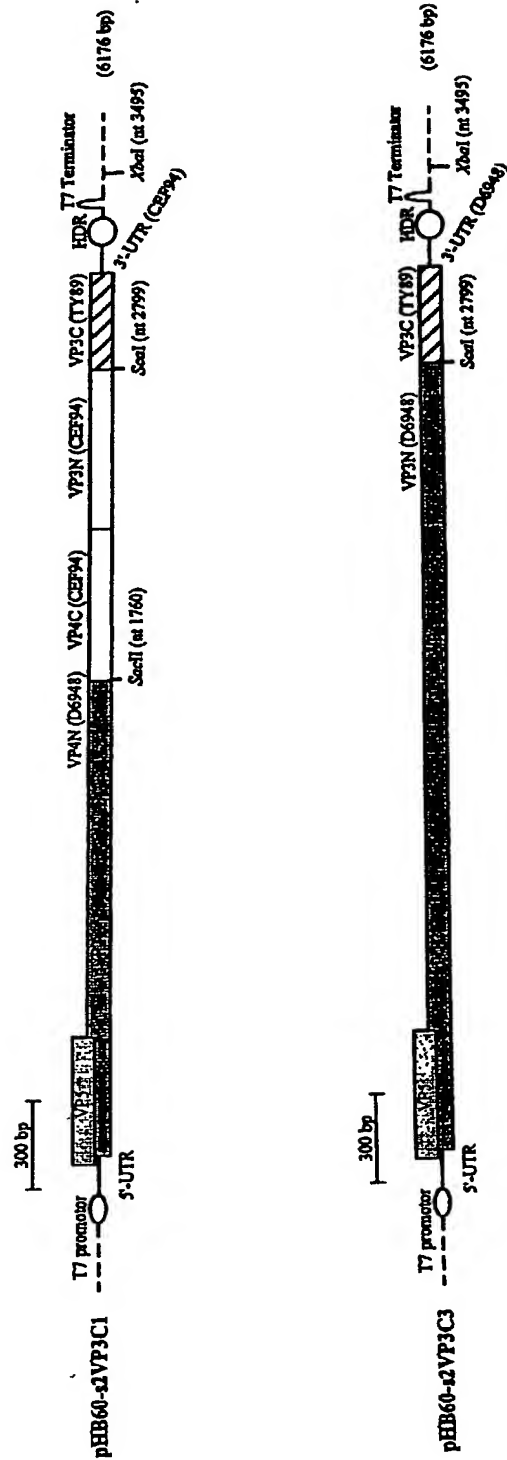
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Fig. 10





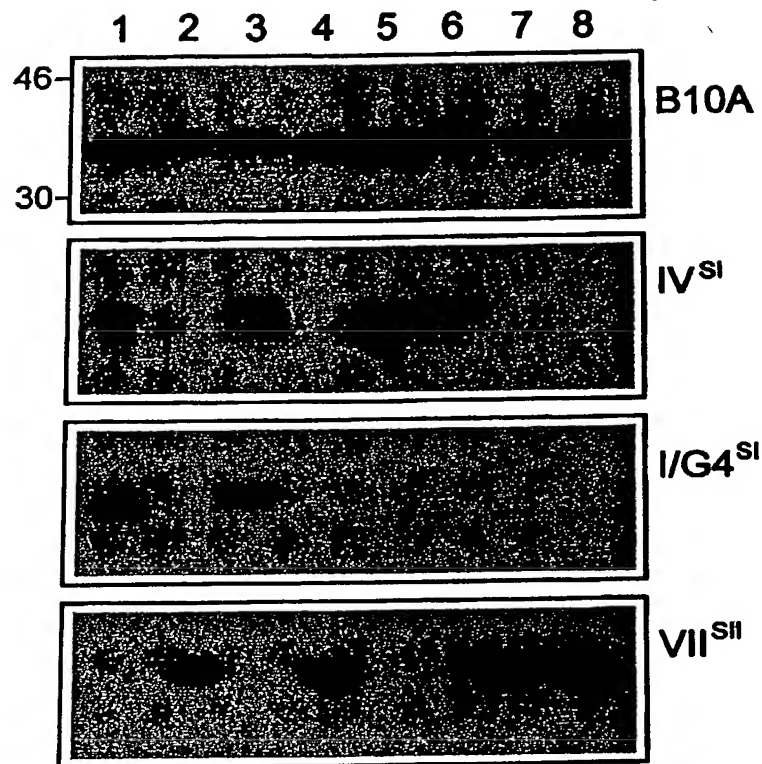
Schematic representation of plasmids pHB60-s2VP3C1 and pHB60-s2VP3C3



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**Fig. 12**



**Fig. 13**

**VP4**  $\longleftrightarrow$  **VP3**

Fig. 14

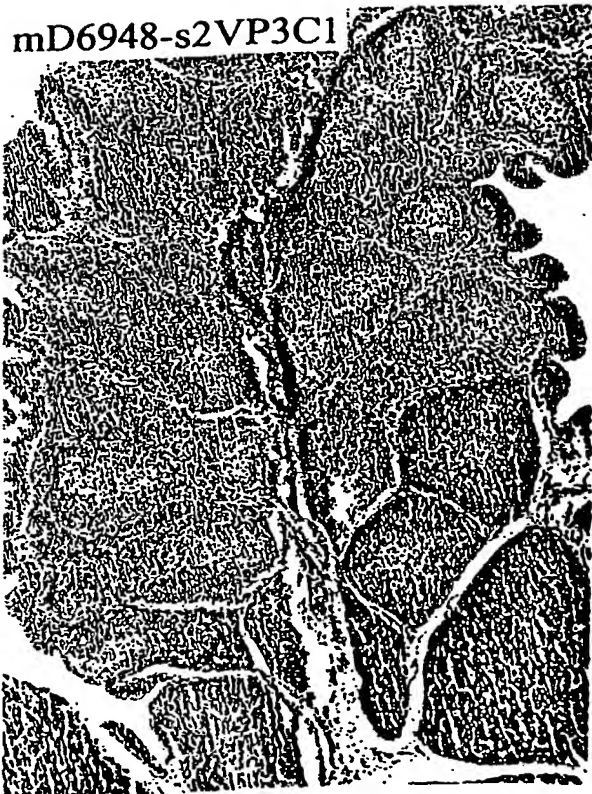
Mock



D6948



mD6948-s2VP3C1

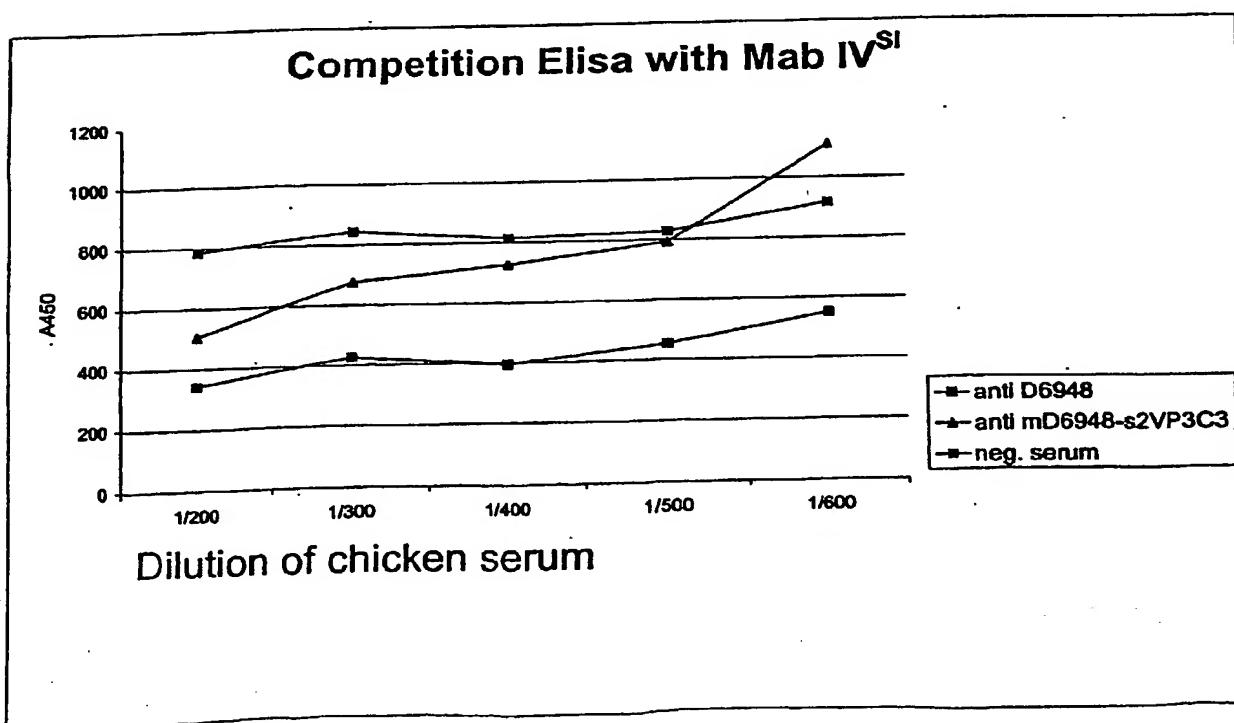
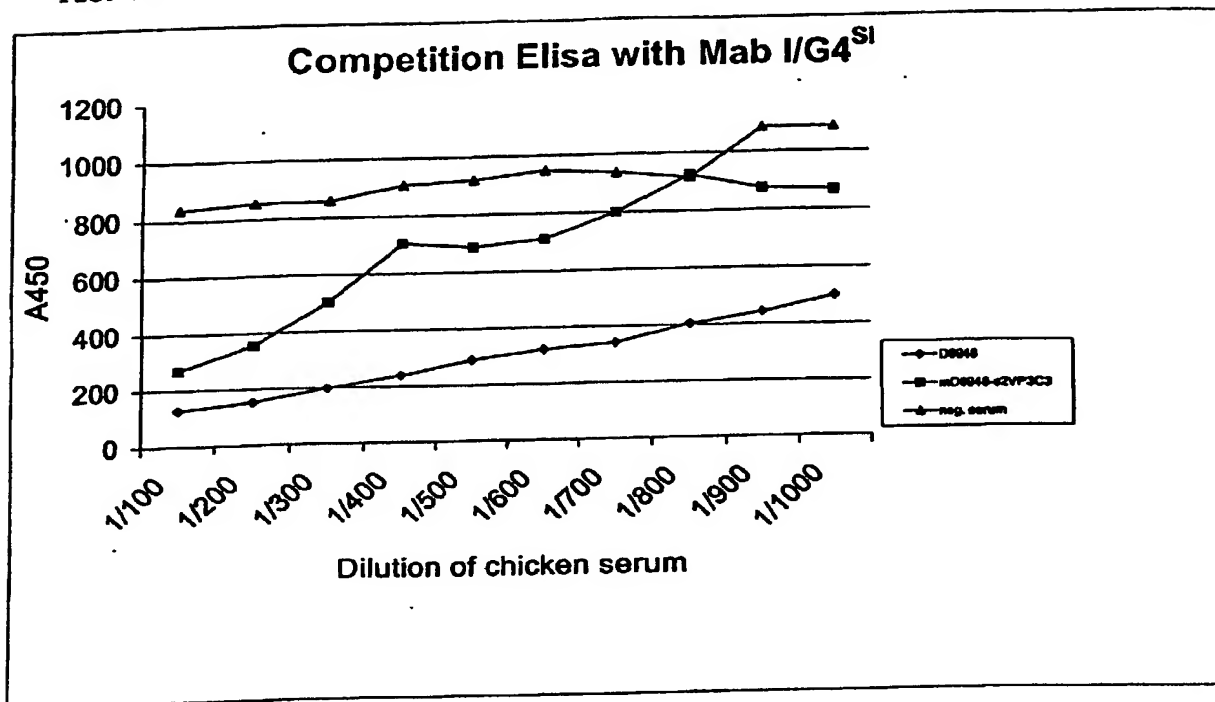


mD6948-s2VP3C3



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FIG. 15



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Fig. 16A

D6948-VP5	MLSLMVSRDQ	TNDRSDDDEA	RSNPTDCSVH	TEPSDANNRT	GVHSGRHPRE	AHSQVRDLDL	QFDCGGRVR	ANCLF	75
CEF94-VP5	-----	K			G				71
	PWFPLNCGC	SLHTAEQWEL	QVRSDAPDCP	EPTGQLQLLQ	ASESESHSEV	KHTPWRLCT	KNEHKRRDLP	RKPE	149
	I			S		R			145

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Fig. 16B

D6948-PP MTNLQDQTQQ IVPFIRSLM PTTGPASIPD DTLEKHTLS ETSTYNLTVG DTGSGLIFFF PGPPGSIVGA HYTLQ 75  
CEF94-PP SNGNYKFDQM LLTAQNLPAS YNYCRLVRS LTVRSSTLPG GUYALNGTIN AVTFQGSLSL LTDVSYNGLM SATAN 150  
INDKIGNVLV GBGVTVLSLP TSYDLGVRL GDPIPAIGLD PKMVATCDSS DRPRVYTITA ADDYQFSSQY QAGGV 225  
TITLFSANID AITSLSIGGE LVFQTSVQGL ILGATIIYILIG FCGTAVITRA VAADNGLTAG TDNLMPFNIV IPTSE 300  
ITQPITSIKL EIVTSKSGGQ AGDQMSWSAS GSLAVTIHGG NYPGALRPVT LVAYERVATG SVTVVAGVSN FELIP 375  
NPFLAKNLVT EYGRFDPGAM NYTKLILSER DRIGIKTVWP TREYTDFFREY FMEVADLNSP LKIAGAFGFK DIIRA 450  
LRRJAVPVVS TLPPPAAPLA HAIGEGVDYL LGDEAQAASG TARABSGKAR AASGRIROLT LAADKGYEVV ANLEQ 525  
VPONPVADGI LASPGLIRGA HNLDCLVREG ATLEFVVLTT VEDAMTPKAL NKKMEAVIEG VREDOLOPESQ RGSEI 600  
RTLSGHRVYG YAPDGVLPDZ TGRDYTVVPI DDVHDDSIML SKDPIPIVNG NSENLATAYM DVERPKVPIH VAMTG 675  
ALNAYGEIEN VSEFSTKLAT AHRIGLKLKAG EGAFDVNIGS NWATFIKRP ENPRDMDRLP YLNLPLYLPN AGROY 750  
DLAMAASEFK ETPELESVR AMEAAANVDP LFQSALSVM WLENGIUTD MANTALSDFN AHRMNFILAN APQAG 825  
SKSQRAKYGT AGYGVREARCP TPPEAQREKD TRISKXMETM GIYPATPEWV ALNGHRGPPSP GOLKYWONTR EIPDP 900  
NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APQAEPPQA FIDEVAKVYE INEGRGPNQE QMKDILLITAM EMKHR 975  
NPRRAPPKPK PKVNAPTQRP PGRIGRWIRA VSEDELE 1012

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Fig. 16C

D6948-VPI  
CEP94-VPI

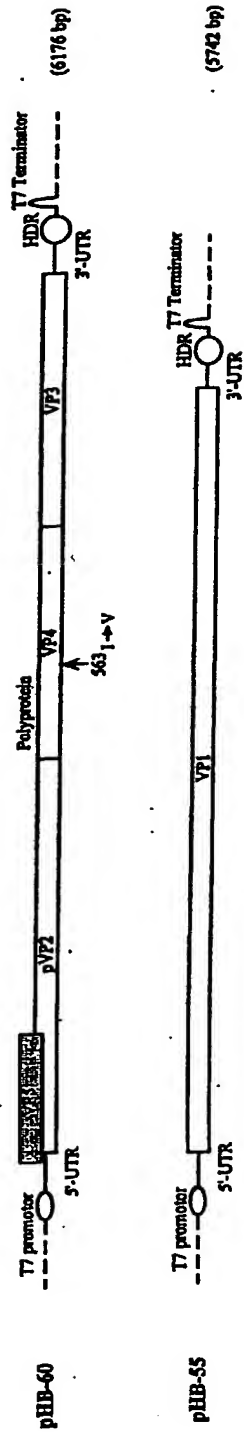
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I T V  
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N EQ  
EVTLLTQNR DRXGSGTYM GQATRLVAMK EVATGRPNPK DPLKLGTYFE SIAQLDITL PVGPPGQDDK PNVPL 225  
TRVPSRMLVL TGDVDGEFEV EDYLPKINLK SSSGLPVVGR TKGETIGEMI AISNQFLREL SALLKQDAGT KGSNK 300  
D T  
KKLLSMLSDY WYLSGGLLFP KAERYDKSTM LTKTRNIWSA PSPTHLMISM ITWPMNSNP NNVLNIEGCP SLYKF 375  
NPFRGGLNRI VENIMAPDEP KALVYADNIY IVHSNTWYSI DLEKGEANCT RQENQAAMYI ILTRGWSNDG DPMFN 450  
L E  
QTWATFAMNI APALVVDSSC LIMNLQIKTY GQSGNAATF INNELLSTLV LDQNNLMKQP SPDSEEFKSI EDKLG 525  
R R  
INFKIERID DIRGKLRQLV PLAQPGLYLSG GVEPEQPST VELDLGWSA TYSKDLGIYV PVLDKERLFC SAAYP 600  
L S  
KGVENKSLKS KVGIEQAYKV VRYEALRLVG GMYPLINKA CKNNASAARR HLEAKGFPLD EFLAENSELS EFGEA 675  
G  
FEGFNKLTV TPESLAEINR PVPPKPPNVN RPNVTGGLKA VSNALKTGRY RNEAGLSGLV LLATARSRLQ DAVKA 750  
S K  
KABAEKLHKS KPDDPDADMF ERSETLSDLL EKADIASKVA HSALVETSDA LEAVQSTSVY TPKYPEVKNP QTASN 825  
879  
881  
PVVGLHLPK RATGVQAALL GAGTERPMGM EAPTRSKNAV KAKRRQRQK ESRQ--  
QP



TITLE: MOSAIC INFECTIOUS BURSAL  
DISEASE VIRUS VACCINES  
Inventor: Boot et al.  
Serial No.: 10/046,671  
Docket No.: 2183-5238US

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Fig. 17



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Fig. 18c

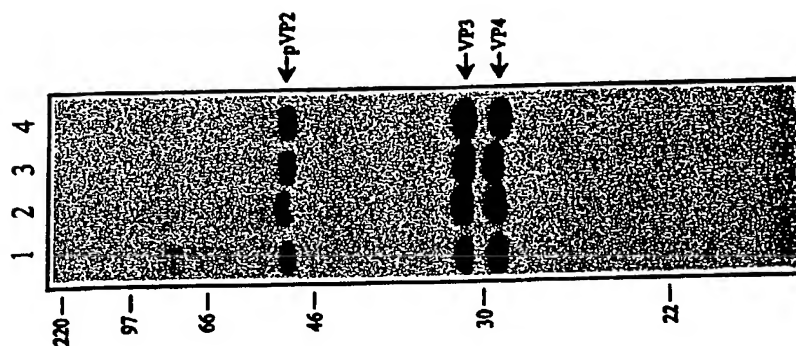


Fig. 18b

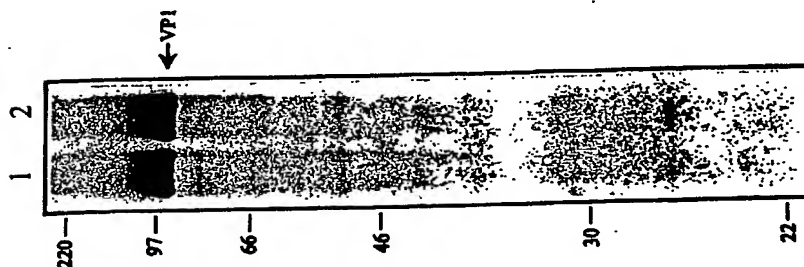
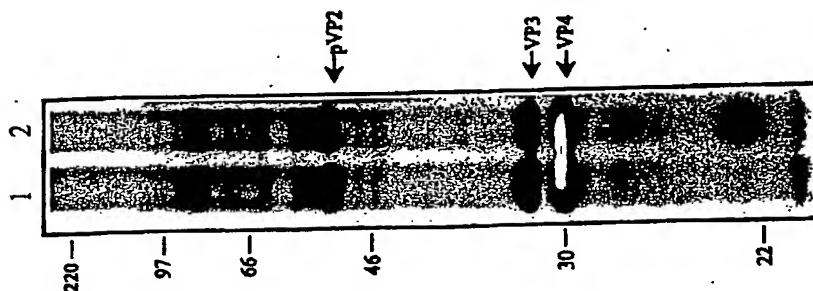
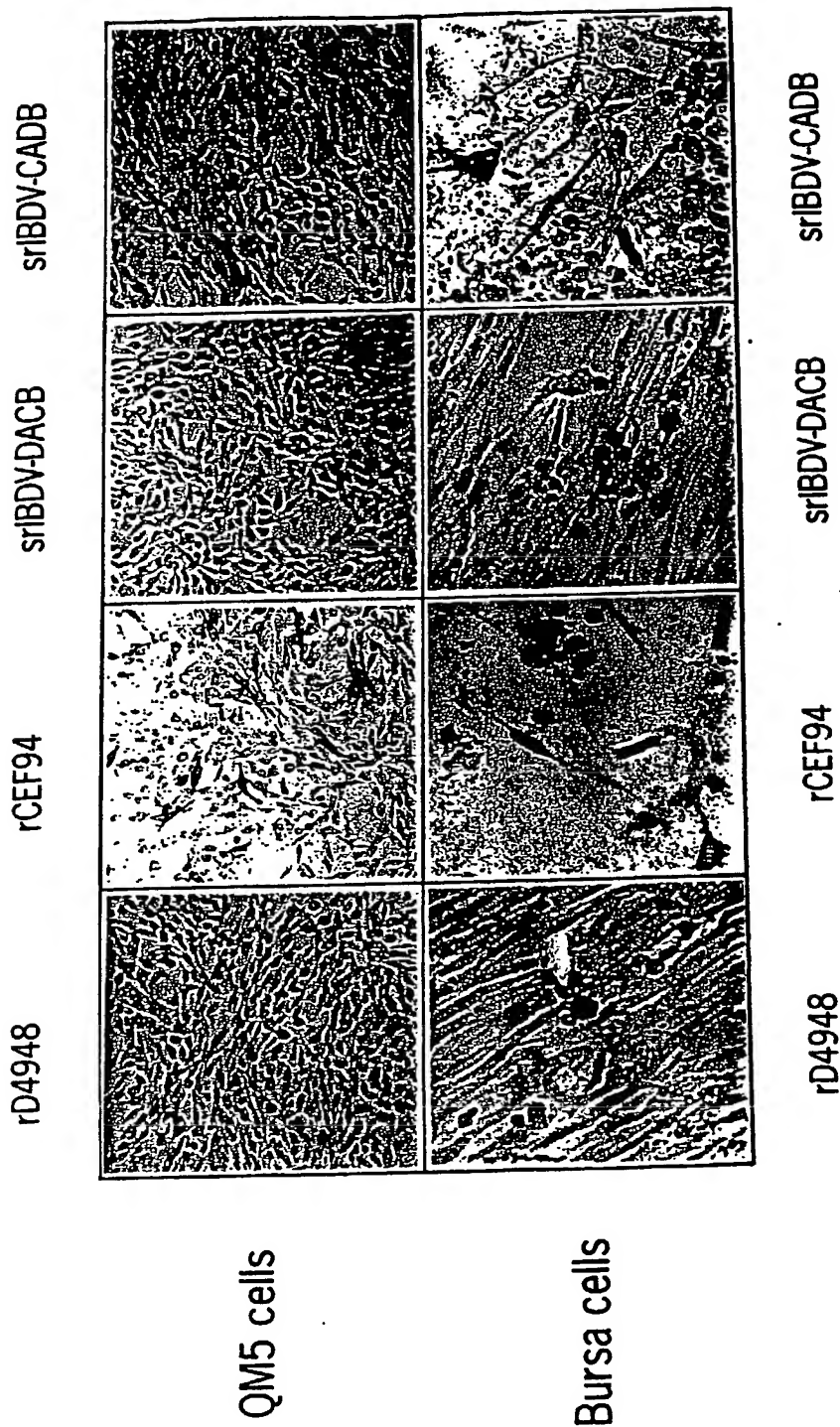


Fig. 18a



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Fig. 19



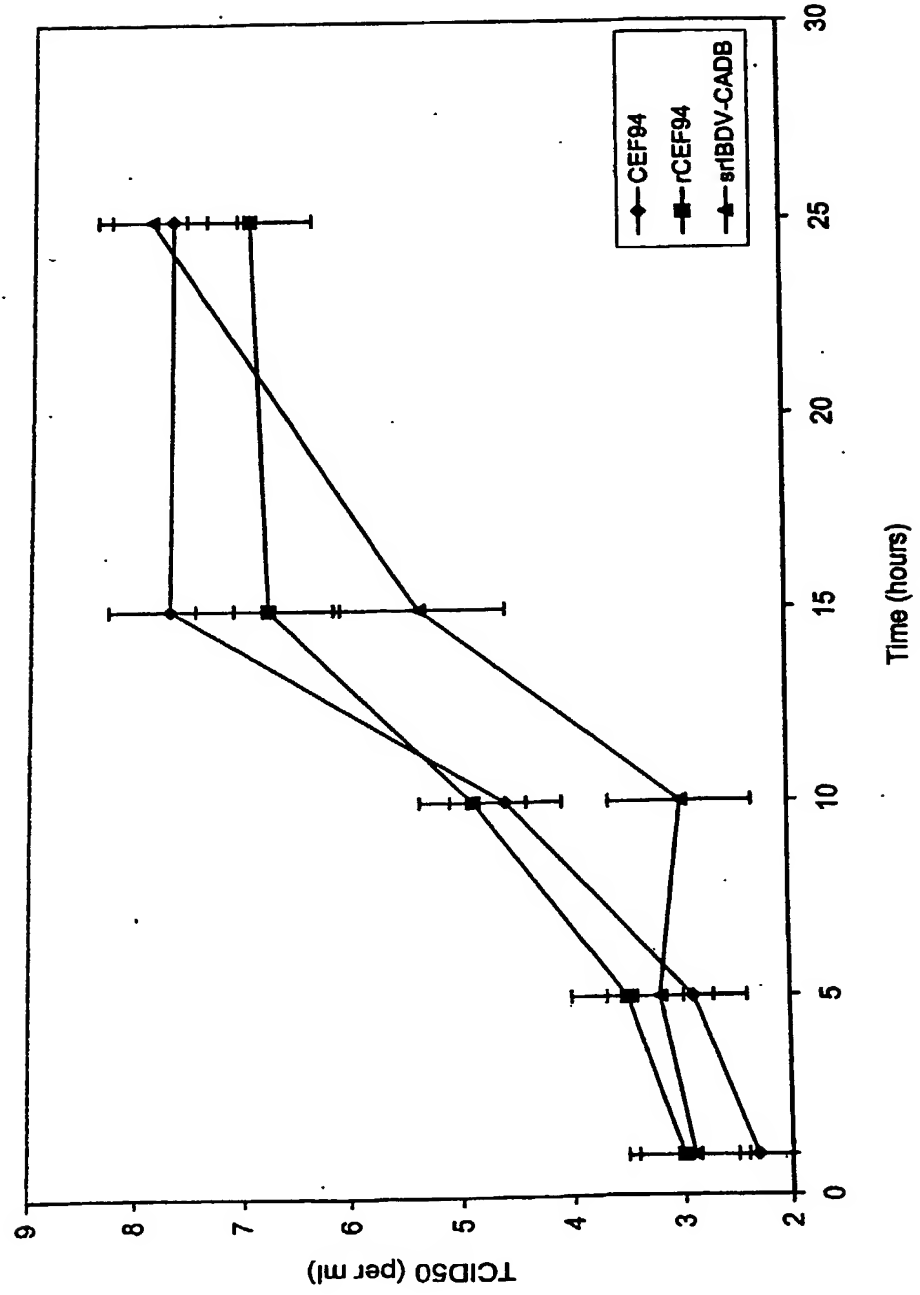


Fig. 20

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Fig. 21

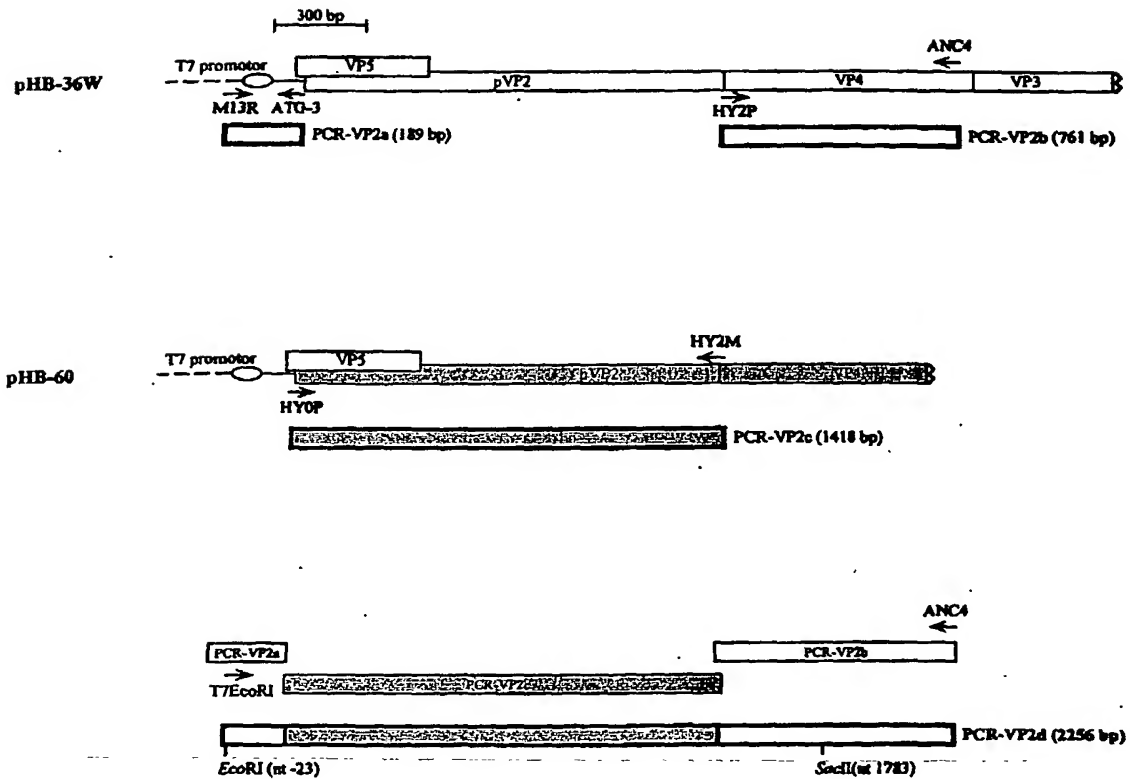


Fig. 22

